

SEQUENCE LISTING

<110> Ledbetter, Jeffrey
Hayden-Ledbetter, Martha

<120> DNA VACCINES ENCODING ANTIGEN LINKED TO A DOMAIN THAT BINDS CD40

<130> US 60/159,690

<140> US 60/159,690
<141> 1999-10-14

<150> US 60/159,690
<151> 1999-10-14

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<170> PatentIn version 3.0

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 <223> Synthetic secretory signal peptide
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 Binds to CD40
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09637864-101300

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 <223> HIV gp 120 allele + ProAspPro linker

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 Binds CD40

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 <223> HIV gp120 + (gly4ser)3 linker

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 short form from amino acids 108-261+Glu
 binds to CD40

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 gtcacagtct attatggggg acctgtgtgg agagaagcaa ccaccactct attttgtgca 180
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 <223> HIV gp120 + ProAspPro linker

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 <222> (1552)..(2028)
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 short form (amino acids 108-261)+Glu
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 <222> (208)..(865)
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 long form from amino acids 48-261+Glu
 binds CD40

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<223> HIV gp120 V3 loop plus ProAspPro linker

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      short form from amino acids 108-261+Glu
      binds CD40

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 short form from amino acids 108-261+Glu
 binds to CD40

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 gggcaacaat ccattcactt gggaggagta tttgaattgc aaccagggtgc ttcggtgttt 600
 gtcaatgtga ctgatccaag ccaagtgagc catggcactg gcttcacgtc ctttggctta 660
 ctcaaactcg agtgataatc taga 684

<210> 20
 <211> 742
 <212> PRT
 <213> HIV-HUMAN FUSION PROTEIN

<220>
 <221> SIGNAL
 <222> (1)..(20)
 <223> synthetic secretory signal peptide

<220>

<221> DOMAIN
 <222> (21)..(526)
 <223> HIV gp120 domain with (gly4ser)3 linker

<220>
 <221> BINDING
 <222> (529)..(742)
 <223> CD154 extracellular domain
 long form from amino acids 48 (Arg) to 261 (Leu)+Glu

<400> 20

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Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
1          5          10          15
Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr
20          25          30
Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Glu
35          40          45
Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr
50          55          60
Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro
65          70          75          80
Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn Phe Asn Met
85          90          95
Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu
100         105         110
Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val
115         120         125
Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr Thr Asn Pro
130         135         140
Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile Lys Asn Cys
145         150         155         160
Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys Lys Glu Tyr
165         170         175
Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn Thr Asn Asn
180         185         190
Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala
195         200         205
Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr Cys Val Pro
210         215         220
Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Ser
225         230         235         240
Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg
245         250         255
Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu
260         265         270

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Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala Lys Thr Ile
 275 280 285
 Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr Arg Pro Asn
 290 295 300
 Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
 305 310 315 320
 Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
 325 330 335
 Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val Ile Lys Leu
 340 345 350
 Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln Ser Ser Gly
 355 360 365
 Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe
 370 375 380
 Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp Asn Val Thr
 385 390 395 400
 Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr Leu Gln Cys
 405 410 415
 Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala Met
 420 425 430
 Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr
 435 440 445
 Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu Thr Glu Thr
 450 455 460
 Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser
 465 470 475 480
 Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile Gly Val Ala
 485 490 495
 Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys Arg Gly Gly
 500 505 510
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Pro Arg
 515 520 525
 Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
 530 535 540
 Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
 545 550 555 560
 Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
 565 570 575
 Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu
 580 585 590
 Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
 595 600 605
 Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
 610 615 620

65					70					75					80
Asn	Pro	Gln	Glu	Val	Val	Leu	Gly	Asn	Val	Thr	Glu	Asn	Phe	Asn	Met
				85					90					95	
Trp	Lys	Asn	Asn	Met	Val	Asp	Gln	Met	His	Glu	Asp	Ile	Ile	Ser	Leu
		100						105					110		
Trp	Asp	Glu	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val
		115					120					125			
Thr	Leu	Asn	Cys	Thr	Asn	Leu	Asn	Ile	Thr	Lys	Asn	Thr	Thr	Asn	Pro
	130					135					140				
Thr	Ser	Ser	Ser	Trp	Gly	Met	Met	Glu	Lys	Gly	Glu	Ile	Lys	Asn	Cys
145					150					155					160
Ser	Phe	Tyr	Ile	Thr	Thr	Ser	Ile	Arg	Asn	Lys	Val	Lys	Lys	Glu	Tyr
				165					170					175	
Ala	Leu	Phe	Asn	Arg	Leu	Asp	Val	Val	Pro	Ile	Glu	Asn	Thr	Asn	Asn
			180					185					190		
Thr	Lys	Tyr	Arg	Leu	Ile	Ser	Cys	Asn	Thr	Ser	Val	Ile	Thr	Gln	Ala
		195					200					205			
Cys	Pro	Lys	Val	Ser	Phe	Gln	Pro	Ile	Pro	Ile	His	Tyr	Cys	Val	Pro
	210					215					220				
Ala	Gly	Phe	Ala	Met	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Ser
225					230					235					240
Gly	Pro	Cys	Thr	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg
				245					250					255	
Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu
			260					265					270		
Asp	Ile	Val	Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asp	Asn	Ala	Lys	Thr	Ile
		275					280					285			
Ile	Val	Gln	Leu	Asn	Glu	Ser	Val	Val	Ile	Asn	Cys	Thr	Arg	Pro	Asn
	290					295					300				
Asn	Asn	Thr	Arg	Arg	Arg	Leu	Ser	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr
305					310					315					320
Ala	Arg	Arg	Asn	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile
				325					330					335	
Ser	Arg	Ala	Lys	Trp	Asn	Asn	Thr	Leu	Gln	Gln	Ile	Val	Ile	Lys	Leu
			340					345					350		
Arg	Glu	Lys	Phe	Arg	Asn	Lys	Thr	Ile	Ala	Phe	Asn	Gln	Ser	Ser	Gly
		355					360					365			
Gly	Asp	Pro	Glu	Ile	Val	Met	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe
	370					375					380				
Phe	Tyr	Cys	Asn	Thr	Ala	Gln	Leu	Phe	Asn	Ser	Thr	Trp	Asn	Val	Thr
385					390					395					400
Gly	Gly	Thr	Asn	Gly	Thr	Glu	Gly	Asn	Asp	Ile	Ile	Thr	Leu	Gln	Cys
				405					410					415	

09037064.101300

Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala Met
 420 425 430
 Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr
 435 440 445
 Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu Thr Glu Thr
 450 455 460
 Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser
 465 470 475 480
 Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile Gly Val Ala
 485 490 495
 Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys Arg Pro Asp
 500 505 510
 Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp
 515 520 525
 Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser
 530 535 540
 Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe
 545 550 555 560
 Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser
 565 570 575
 Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
 580 585 590
 Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
 595 600 605
 Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly
 610 615 620
 Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
 625 630 635 640
 Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile
 645 650 655
 Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu
 660 665 670
 Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser
 675 680 685
 Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe
 690 695 700
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 705 710 715 720
 Ser Phe Gly Leu Leu Lys Leu Glu
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<210> 22
 <211> 682
 <212> PRT
 <213> HIV-HUMAN FUSION PROTEIN

<220>
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 <222> (1)..(20)
 <223> Synthetic secretory signal peptide

<220>
 <221> DOMAIN
 <222> (21)..(525)
 <223> HIV gp120 domain plus (gly4ser)3 linker

<220>
 <221> DOMAIN
 <222> (528)..(682)
 <223> CD154 extracellular domain
 short form from amino acids 108 (Glu) to 261 (Leu)+Glu
 Binds CD40

<400> 22

Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
 1 5 10 15
 Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr
 20 25 30
 Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Glu
 35 40 45
 Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr
 50 55 60
 Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro
 65 70 75 80
 Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn Phe Asn Met
 85 90 95
 Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu
 100 105 110
 Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val
 115 120 125
 Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr Thr Asn Pro
 130 135 140
 Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile Lys Asn Cys
 145 150 155 160
 Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys Lys Glu Tyr
 165 170 175
 Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn Thr Asn Asn
 180 185 190
 Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala
 195 200 205
 Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr Cys Val Pro
 210 215 220
 Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Ser

225		230		235		240									
Gly	Pro	Cys	Thr	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg
				245					250					255	
Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu
			260					265					270		
Asp	Ile	Val	Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asp	Asn	Ala	Lys	Thr	Ile
		275					280					285			
Ile	Val	Gln	Leu	Asn	Glu	Ser	Val	Val	Ile	Asn	Cys	Thr	Arg	Pro	Asn
	290					295					300				
Asn	Asn	Thr	Arg	Arg	Arg	Leu	Ser	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr
305					310					315					320
Ala	Arg	Arg	Asn	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile
				325					330					335	
Ser	Arg	Ala	Lys	Trp	Asn	Asn	Thr	Leu	Gln	Gln	Ile	Val	Ile	Lys	Leu
			340					345					350		
Arg	Glu	Lys	Phe	Arg	Asn	Lys	Thr	Ile	Ala	Phe	Asn	Gln	Ser	Ser	Gly
		355					360					365			
Gly	Asp	Pro	Glu	Ile	Val	Met	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe
	370					375					380				
Phe	Tyr	Cys	Asn	Thr	Ala	Gln	Leu	Phe	Asn	Ser	Thr	Trp	Asn	Val	Thr
385					390					395					400
Gly	Gly	Thr	Asn	Gly	Thr	Glu	Gly	Asn	Asp	Ile	Ile	Thr	Leu	Gln	Cys
				405					410					415	
Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met	Trp	Gln	Lys	Val	Gly	Lys	Ala	Met
			420					425					430		
Tyr	Ala	Pro	Pro	Ile	Thr	Gly	Gln	Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr
		435					440					445			
Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	Gly	Asn	Ser	Thr	Glu	Thr	Glu	Thr
	450					455					460				
Glu	Ile	Phe	Arg	Pro	Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser
465					470					475					480
Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Arg	Ile	Glu	Pro	Ile	Gly	Val	Ala
				485					490					495	
Pro	Thr	Arg	Ala	Lys	Arg	Arg	Thr	Val	Gln	Arg	Glu	Lys	Arg	Gly	Gly
			500					505					510		
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Pro	Glu
		515					520					525			
Asn	Ser	Phe	Glu	Met	Gln	Lys	Gly	Asp	Gln	Asn	Pro	Gln	Ile	Ala	Ala
	530					535					540				
His	Val	Ile	Ser	Glu	Ala	Ser	Ser	Lys	Thr	Thr	Ser	Val	Leu	Gln	Trp
545					550					555					560
Ala	Glu	Lys	Gly	Tyr	Tyr	Thr	Met	Ser	Asn	Asn	Leu	Val	Thr	Leu	Glu
				565					570					575	

Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr
 580 585 590

Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro
 595 600 605

Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile
 610 615 620

Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln
 625 630 635 640

Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser
 645 650 655

Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly
 660 665 670

Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
 675 680

<210> 23
 <211> 668
 <212> PRT
 <213> HIV-HUMAN FUSION PROTEIN

<220>
 <221> SIGNAL
 <222> (1)..(20)
 <223> Synthetic secretory signal peptide

<220>
 <221> DOMAIN
 <222> (21)..(513)
 <223> HIV gp120 domain with ProAspPro linker

<220>
 <221> BINDING
 <222> (514)..(668)
 <223> CD154 extracellular domain
 short form from amino acids 108 (Glu) to 261 (Leu)+Glu
 Binds to CD40

<400> 23

Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
 1 5 10 15

Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr
 20 25 30

Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Glu
 35 40 45

Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr
 50 55 60

Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro
 65 70 75 80

Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn Phe Asn Met
 85 90 95

435 440 445
 Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu Thr Glu Thr
 450 455 460
 Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser
 465 470 475 480
 Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile Gly Val Ala
 485 490 495
 Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys Arg Pro Asp
 500 505 510
 Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile
 515 520 525
 Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu
 530 535 540
 Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr
 545 550 555 560
 Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr
 565 570 575
 Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln
 580 585 590
 Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu
 595 600 605
 Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys
 610 615 620
 Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly
 625 630 635 640
 Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly
 645 650 655
 Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
 660 665

<210> 24
 <211> 294
 <212> PRT
 <213> HIV-HUMAN FUSION PROTEIN

<220>
 <221> SIGNAL
 <222> (1)..(20)
 <223> Synthetic secretory signal peptide

<220>
 <221> DOMAIN
 <222> (21)..(77)
 <223> HIV gp120 V3 loop plus (gly4ser)3 linker

<220>
 <221> BINDING
 <222> (80)..(294)
 <223> CD154 extracellular domain

long form from amino acids 48 (Arg) to 261 (Leu)+Glu
binds CD40

<400> 24

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Met  Leu  Tyr  Thr  Ser  Gln  Leu  Leu  Gly  Leu  Leu  Leu  Phe  Trp  Ile  Ser
1      5      10      15
Ala  Ser  Arg  Ser  Val  Val  Ile  Asn  Cys  Thr  Arg  Pro  Asn  Asn  Asn  Thr
20      25      30
Arg  Arg  Arg  Leu  Ser  Ile  Gly  Pro  Gly  Arg  Ala  Phe  Tyr  Ala  Arg  Arg
35      40      45
Asn  Ile  Ile  Gly  Asp  Ile  Arg  Gln  Ala  His  Cys  Asn  Ile  Ser  Gly  Gly
50      55      60
Gly  Gly  Ser  Gly  Gly  Gly  Gly  Ser  Gly  Gly  Gly  Gly  Ser  Asp  Pro  Arg
65      70      75      80
Arg  Leu  Asp  Lys  Ile  Glu  Asp  Glu  Arg  Asn  Leu  His  Glu  Asp  Phe  Val
85      90      95
Phe  Met  Lys  Thr  Ile  Gln  Arg  Cys  Asn  Thr  Gly  Glu  Arg  Ser  Leu  Ser
100     105     110
Leu  Leu  Asn  Cys  Glu  Glu  Ile  Lys  Ser  Gln  Phe  Glu  Gly  Phe  Val  Lys
115     120     125
Asp  Ile  Met  Leu  Asn  Lys  Glu  Glu  Thr  Lys  Lys  Glu  Asn  Ser  Phe  Glu
130     135     140
Met  Gln  Lys  Gly  Asp  Gln  Asn  Pro  Gln  Ile  Ala  Ala  His  Val  Ile  Ser
145     150     155     160
Glu  Ala  Ser  Ser  Lys  Thr  Thr  Ser  Val  Leu  Gln  Trp  Ala  Glu  Lys  Gly
165     170     175
Tyr  Tyr  Thr  Met  Ser  Asn  Asn  Leu  Val  Thr  Leu  Glu  Asn  Gly  Lys  Gln
180     185     190
Leu  Thr  Val  Lys  Arg  Gln  Gly  Leu  Tyr  Tyr  Ile  Tyr  Ala  Gln  Val  Thr
195     200     205
Phe  Cys  Ser  Asn  Arg  Glu  Ala  Ser  Ser  Gln  Ala  Pro  Phe  Ile  Ala  Ser
210     215     220
Leu  Cys  Leu  Lys  Ser  Pro  Gly  Arg  Phe  Glu  Arg  Ile  Leu  Leu  Arg  Ala
225     230     235     240
Ala  Asn  Thr  His  Ser  Ser  Ala  Lys  Pro  Cys  Gly  Gln  Gln  Ser  Ile  His
245     250     255
Leu  Gly  Gly  Val  Phe  Glu  Leu  Gln  Pro  Gly  Ala  Ser  Val  Phe  Val  Asn
260     265     270
Val  Thr  Asp  Pro  Ser  Gln  Val  Ser  His  Gly  Thr  Gly  Phe  Thr  Ser  Phe
275     280     285
Gly  Leu  Leu  Lys  Leu  Glu
290

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<210> 25

<211> 280

Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr
 130 135 140
 Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro
 145 150 155 160
 Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile
 165 170 175
 Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln
 180 185 190
 Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser
 195 200 205
 Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly
 210 215 220
 Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
 225 230

<210> 27
 <211> 220
 <212> PRT
 <213> HIV-HUMAN FUSION PROTEIN

 <220>
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 <223> synthetic secretory signal peptide

 <220>
 <221> DOMAIN
 <222> (21)..(65)
 <223> HIV gp120 V3 loop plus ProAspPro linker

 <220>
 <221> BINDING
 <222> (66)..(220)
 <223> CD154 extracellular domain from amino acids 108 (Glu)-261(Leu)+Glu
 Binds CD40

<400> 27

Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
 1 5 10 15
 Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
 20 25 30
 Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr Ala Arg Arg
 35 40 45
 Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Pro Asp
 50 55 60
 Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile
 65 70 75 80
 Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu
 85 90 95

